

GenCore version 5.1.4\_p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 21:32:07 ; Search time 8449.13 Seconds  
(without alignments)  
117.112 Million cell updates/sec

Title: US-09-913-524-33

Perfect score: 34

Sequence: 1 aggcctccggagggaacnctgcccacgaact 34

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl :

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pi.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vt.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pi.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vt.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rtd.\*
- 36: em\_htg\_nam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	33	97.1	847	9	HSINHAG2
2	33	97.1	1134	6	A14420
3	33	97.1	1237	6	I01843
4	33	97.1	1237	6	I05264
5	33	97.1	1237	6	I21913
6	33	97.1	1237	6	I64619
7	33	97.1	1237	6	I87901
8	33	97.1	1237	9	HUMINHA
9	33	97.1	1237	6	I00529
10	33	97.1	1338	9	HUMINHA
11	33	97.1	1338	9	BC006391
12	33	97.1	53239	2	AC011971
13	33	97.1	135033	9	AC009955
14	33	97.1	182662	2	AC024009
15	33	97.1	186883	2	AC040991
16	26.6	78.2	994	4	EC021219
17	26.6	78.2	1144	10	RATINHAB2
18	26.6	78.2	1286	4	HRSIASP
19	26.6	78.2	1372	10	AF432351
20	26.6	78.2	1561	10	RATINHA
21	26.6	78.2	101356	2	AC112361
22	25	73.5	857	4	SHPINHA
23	25	73.5	1160	10	MMINAS
24	25	73.5	1182	4	BOVINHA
25	25	73.5	1183	5	A14416
26	25	73.5	1183	10	MUSINHIB02
27	25	73.5	1328	10	NNALPHA
28	23.4	68.8	731	4	AY028465
29	23.4	68.8	731	4	AY028466
30	23.4	68.8	1272	4	PTGINHA
31	23.4	68.8	1333	4	SSINHAR
32	23.4	68.8	1343	6	I01835
33	23.4	68.8	1343	6	I05231
34	23.4	68.8	1343	6	I21910
35	23.4	68.8	1343	6	I64616
36	23.4	68.8	1343	6	I87898
37	22	64.7	237982	2	AC093483
38	21.6	63.5	180525	2	AC104750
39	21.6	63.5	187740	2	AC126863
40	21	61.8	162328	9	AP000350
41	21	61.8	236809	2	AC103535
42	20.8	61.2	5108	9	HSN802883
43	20.8	61.2	5145	6	AX127534
44	20.8	61.2	5145	9	AB037848
45	20.8	61.2	11158	1	AE004682

ALIGNMENTS

RESULT 1	HSINHAG2	H.sapiens inhA gene, exon 2.	847 bp	DNA	linear	PRI 10-FEB-1997
LOCUS	X04446					
DEFINITION	X04446.1	GI:33924				
ACCESSION	X04446.1					
VERSION	X04446.1					
KEYWORDS	glycoprotein; glycoprotein hormone; hormone; inhibin; preprohormone.					
SOURCE	Homo sapiens					
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 847)					
AUTHORS	Stewart,A.G., Milborrow,H.M., Ring,J.M., Crowther,C.E. and Forage,R.G.					

TITLE Human inhibin genes. Genomic characterisation and sequencing  
 JOURNAL FEBS Lett. 206 (2), 329-334 (1986)  
 MEDLINE 87005283  
 PUBMED 3758355  
 COMMENT See X04445 for exon 1.  
 DATA kindly reviewed (05-JAN-1986) by Stewart A.  
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 /number=2  
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 /usedin=X04445:inh\_mrna  
 172..174  
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 538..540  
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 640..642  
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 /note="pot. N-glycosylation site"  
 BASE COUNT 136 a 307 c 233 g 171 t  
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 QY 1 AGGCCTCCGAGGAGAACCGNCTGCCATGCCCACT 34  
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 DB 487 AGGCCTCCGAGGAGAACCGCTGCCATGCCCACT 520  
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 RESULT 2  
 A14420  
 LOCUS A14420 1134 bp DNA linear PAT 09-FEB-1994  
 DEFINITION Inhibin A subunit.  
 ACCESSION A14420  
 VERSION A14420.1 GI:490129  
 KEYWORDS  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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 /db\_xref="SWISS-PROT:P05111"  
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 AVTREGEDPVRRLPRHALGFTTHRGSEPEEEDVSQALIFPATDASCEPKSAARGL  
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 GPVAVPMSLGHAPHWAVLHLATLSALLTHPVLLLRCLPTCSARPEATPLFLVH  
 TRTRPPSGGERAPRSTPLMSWPSPSALRLIQRPEEPAHANCHERVALNISTQELGW  
 ERWIVPPSIFLHYCHGCGGLHIPPNLISLPVGPAPTPAQPYSLLPQPCCAALPOT  
 MRPLHRTISDGGISFKYETVPNLLTQHCACI"  
 BASE COUNT 182 a 396 c 326 g 230 t  
 ORIGIN  
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Best Local Similarity 97.1%; Pred. No. 0.0097;  
 Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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 DB 758 AGGCCTCCGAGGAGAACCGCTGCCATGCCCACT 791  
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 RESULT 3  
 I01843  
 LOCUS I01843 1237 bp ss-DNA linear PAT 21-MAY-1993  
 DEFINITION Sequence 10 from Patent US 479885.  
 ACCESSION I01843  
 VERSION I01843.1 GI:269775  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 1237)  
 AUTHORS Mascot, A.J. and Seeburg, P.H.  
 TITLE Compositions of hormonally active human and porcine inhibin  
 containing an alpha chain and 62 chai.  
 JOURNAL Patent: US 479885-A 10 17-JAN-1989;  
 Genentech, Inc.; South San Francisco, CA  
 FEATURES  
 source 1..1237  
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 ORIGIN  
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 Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 AGGCCTCCGAGGAGAACCGNCTGCCATGCCCACT 34  
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 DB 708 AGGCCTCCGAGGAGAACCGCTGCCATGCCCACT 741  
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 RESULT 4  
 I05264  
 LOCUS I05264 1237 bp DNA linear PAT 02-DEC-1994  
 DEFINITION Sequence 21 from Patent EP 0222491.  
 ACCESSION I05264  
 VERSION I05264.1 GI:591394  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 1237)  
 AUTHORS Mason, A.J. and Seeburg, P.H.  
 TITLE Nucleic acid encoding the alpha or beta chains of inhibin and  
 method for synthesizing polypeptides using such nucleic acid  
 JOURNAL Patent: EP 0222491-A1 21 20-MAY-1987;  
 FEATURES  
 source 1..1237  
 /organism="unknown"  
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 ORIGIN  
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 Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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 DB 708 AGGCCTCCGAGGAGAACCGCTGCCATGCCCACT 741  
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 RESULT 5  
 I21913  
 LOCUS I21913 1237 bp DNA linear PAT 07-OCT-1996  
 DEFINITION Sequence 40 from patent US 5525488.

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ACCESSION      I21913
VERSION        I21913.1  GI:1602267
KEYWORDS
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 1237)
AUTHORS      Mason,A.J. and Seeburg,P.H.
TITLE        Nucleic acid encoding the mature .alpha. chain of inhibin and
              method for synthesizing polypeptides using such nucleic acid
JOURNAL       Patent: US 5525488-A 40 11-JUN-1996;
FEATURES      Location/Qualifiers
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Best Local Similarity 97.1%; Pred. No. 0.0096;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGCTCCGGAGGACCGNCTGCCATGCCAACT 34
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Db 708 AGGCTCCGGAGGACCGNCTGCCATGCCAACT 741

RESULT 6
LOCUS         I64619
DEFINITION    Sequence 40 from patent US 5665568.
ACCESSION     I64619
VERSION       I64619.1  GI:2481513
KEYWORDS
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 1237)
AUTHORS      Mason,A.J. and Seeburg,P.H.
TITLE        Nucleic acid encoding the mature .beta. sub.A chain of inhibin and
              method for synthesizing polypeptides using such nucleic acid
JOURNAL       Patent: US 5665568-A 40 09-SEP-1997;
FEATURES      Location/Qualifiers
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BASE COUNT    210 a 431 c 346 g 250 t
ORIGIN
Query Match   97.1%; Score 33; DB 6; Length 1237;
Best Local Similarity 97.1%; Pred. No. 0.0096;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGCTCCGGAGGACCGNCTGCCATGCCAACT 34
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Db 708 AGGCTCCGGAGGACCGNCTGCCATGCCAACT 741

RESULT 7
LOCUS         I87901
DEFINITION    Sequence 40 from patent US 5716810.
ACCESSION     I87901
VERSION       I87901.1  GI:3407841
KEYWORDS
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 1237)
AUTHORS      Mason,A.J. and Seeburg,P.H.
TITLE        Nucleic acid encoding the mature .beta. sub.B chain of inhibin and
              method for synthesizing polypeptides using such nucleic acid
JOURNAL       Patent: US 5716810-A 40 10-FEB-1996;
FEATURES      Location/Qualifiers
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               1..1237

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BASE COUNT    210 a 431 c 346 g 250 t
ORIGIN
Query Match   97.1%; Score 33; DB 6; Length 1237;
Best Local Similarity 97.1%; Pred. No. 0.0096;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGCTCCGGAGGACCGNCTGCCATGCCAACT 34
|||||
Db 708 AGGCTCCGGAGGACCGNCTGCCATGCCAACT 741

RESULT 8
LOCUS         HUMINHAA
DEFINITION    Human ovarian alpha-inhibin mRNA.
ACCESSION     M13144
VERSION       M13144.1  GI:186412
KEYWORDS
SOURCE        Human polycystic ovarian cDNA to mRNA, clones lambda-hin-alpha-
              [2.6].
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1237)
AUTHORS      Mason,A.J., Niall,H.D. and Seeburg,P.H.
TITLE        Structure of two human ovarian inhibins
JOURNAL       Biochem. Biophys. Res. Commun. 135 (3), 957-964 (1986)
MEDLINE       86186863
PUBMED        3754442
FEATURES      Location/Qualifiers
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               TPLRSWSPSSALRLQRPPEEPAHANCHRVALLSTFQELGWRWIVYPPSTFIHYC
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Best Local Similarity 97.1%; Pred. No. 0.0096;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 708 AGGCTCCGGAGGACCGNCTGCCATGCCAACT 741

RESULT 9
LOCUS         IO0529
DEFINITION    Sequence 1 from Patent US 4737578.
ACCESSION     IO0529
VERSION       IO0529.1  GI:268923
KEYWORDS
SOURCE        Unknown.
ORGANISM      Unknown.

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REFERENCE 1 (bases 1 to 1338)
AUTHORS Evans,R.M., Rosenfeld,M.G., Cerelli,G., Mayo,K.E., Spiess,J.,
        Rivier,J.B.F. and Vale,W.W. Jr.
TITLE Human inhibin
JOURNAL Patent: US 4737578-A 1 12-APR-1988;
        The Salk Institute for Biological Studies; San Diego, CA
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Best local Similarity 97.1%; Pred. No. 0.0096;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGCTCCGGAGGAACGCTGCGCATGCCCAACT 34
    |||||
Db 895 AGGCTCCGGAGGAACGCTGCGCATGCCCAACT 928

RESULT 10
HUMINHA
LOCUS Human inhibin A-subunit mRNA, complete cds. PRI 06-JAN-1995
DEFINITION M13981
ACCESSION M13981
VERSION M13981.1 GI:186410
KEYWORDS inhibin.
SOURCE Human term placenta, cDNA to mRNA, clone hFSA-110.
ORGANISM Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
        Mayo,K.E., Cerelli,G.M., Spiess,J., Rivier,J., Rosenfeld,M.G.,
        Evans,R.M. and Vale,W.
        Inhibin A-subunit cDNAs from porcine ovary and human placenta
        Proc. Natl. Acad. Sci. U.S.A. 83 (16), 5849-5853 (1986)
        86287450
        PUBMED 3016724

FEATURES
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    GPVAPVNSLGHAPPHAVLHATLSALSLLTHPVLVLLRCPLCTCSARPEATPFLVAH
    TRTPPSGGERARRSTPLMSWPWSALRLQRPPEPAHANCHRVAINTSFQELGM
    ERWIVYPPSFIHYHGGCGLLHPNLSLPVPGAPPTPAQPSYLLPGAQPCCAALPGT
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    /note="inhibin A-subunit signal peptide"
    841..1242
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    /product="inhibin A-subunit"
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BASE COUNT 232 a 433 c 417 g 256 t
ORIGIN
Query Match 97.1%; Score 33; DB 9; Length 1338;
Best local Similarity 97.1%; Pred. No. 0.0096;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 11
BC006391
LOCUS Homo sapiens, inhibin, alpha, clone MCC:12547 IMAGE:4126990, mRNA,
DEFINITION complete cds.
ACCESSION BC006391
VERSION BC006391.1 GI:13623556
KEYWORDS MCC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
        Strausberg,K.
        Direct Submission
        Submitted (09-APR-2001) National Institutes of Health, Mammalian
        Gene Collection (MGC), Cancer Genomics Office, National Cancer
        Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
        USA
        NIH-MGC Project URL: http://mgc.nci.nih.gov
        Contact: MCC help desk
        Email: cgaibs-remail.nih.gov
        Tissue Procurement: ATCC
        cDNA Library Preparation: Rubin Laboratory
        cDNA Library Arrayed by: The J.M.A.G.E. Consortium (LLNI,)
        DNA Sequencing by: National Institutes of Health Intramural
        Sequencing Center (NISC),
        Gaithersburg, Maryland.
        Web site: http://www.nisc.nih.gov/
        Contact: nisc.mgc@nih.gov
        Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
        Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
        Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
        Lim,M., Maduro,Q.L., Mastello,C., Mastrian,S.D., McCloskey,J.C.,
        McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
        Tongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
        Zhang,L.-H. and Green,E.D.

Clone distribution: MCC clone distribution information can be found
through the J.M.A.G.E. Consortium/ILNI at: http://image.llnl.gov
Series: IMAGE Plate: 17 Row: h Column: 17
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 9257223.

FEATURES
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    GPVAPVNSLGHAPPHAVLHATLSALSLLTHPVLVLLRCPLCTCSARPEATPFLVAH
    TRTPPSGGERARRSTPLMSWPWSALRLQRPPEPAHANCHRVAINTSFQELGM
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BASE COUNT 258 a 469 c 394 g 272 t
ORIGIN

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Query Match 97.1%; Score 33; DB 9; Length 1393;  
Best Local Similarity 97.1%; Pred. No. 0.0095;  
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QY 1 AGGCTCCGAGGACCGCTCCCATCCCAACT 34  
|||||  
DB 840 AGGCTCCGAGGACCGCTCCCATCCCAACT 873

## RESULT 12

AC011971  
LOCUS Homo sapiens clone RP11-15J2, low-pass sequence sampling.  
DEFINITION AC011971  
ACCESSION AC011971.2 GI:7144910  
VERSION  
KEYWORDS HTG; HTGS-PHASE0.  
SOURCE  
ORGANISM Homo sapiens

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 53239)  
Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
Homo sapiens chromosome, clone RP11-15J2

## REFERENCE

2 (bases 1 to 53239)  
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,  
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,  
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,  
Cooke,P., DeArelano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,  
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J.,  
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,  
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,  
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marguis,N.,  
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,  
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,  
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,  
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,  
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,  
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (17-OCT-1999) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA

## TITLE

On Mar 3, 2000 this sequence version replaced gi:6065396.  
All repeats were identified using RepeatMasker:  
Sait, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RN/RepeatMasker.html>

## COMMENT

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: W1HR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: U3480  
Center clone name: 15\_J2

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\* NOTE: This record contains 59 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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\* 1763 2553: contig of 791 bp in length  
\* 2554 2653: gap of 100 bp

\* 2654 3497: contig of 844 bp in length  
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\* 13467 13566: gap of 100 bp  
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\* 17078 17860: contig of 783 bp in length  
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\* 18842 18941: gap of 100 bp  
\* 18942 19724: contig of 783 bp in length  
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\* 20661 21354: contig of 694 bp in length  
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\* 21455 22269: contig of 815 bp in length  
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\* 23264 24012: contig of 749 bp in length  
\* 24013 24112: gap of 100 bp  
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\* 25881 26672: contig of 792 bp in length  
\* 26673 26772: gap of 100 bp  
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\* 27627 27726: gap of 100 bp  
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\* 28588 28687: gap of 100 bp  
\* 28688 29501: contig of 814 bp in length  
\* 29502 29601: gap of 100 bp  
\* 29602 30332: contig of 731 bp in length  
\* 30333 30432: gap of 100 bp  
\* 30433 31215: contig of 783 bp in length  
\* 31216 31315: gap of 100 bp  
\* 31316 32153: contig of 838 bp in length  
\* 32154 32253: gap of 100 bp  
\* 32254 32926: contig of 673 bp in length  
\* 32927 33026: gap of 100 bp  
\* 33027 33815: contig of 789 bp in length  
\* 33816 33915: gap of 100 bp  
\* 33916 34761: contig of 846 bp in length  
\* 34762 34861: gap of 100 bp  
\* 34862 35683: contig of 822 bp in length



overlap. Actual start of this clone is at base position 1 of  
RP11-256123; actual end is at base position 52326 of RP11-51207.

FEATURES

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Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 14

AC024009

LOCUS

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Homo sapiens chromosome 2 clone RP11-158J14 map 2, WORKING DRAFT  
SEQUENCE, 30 unordered pieces.

ACCESSION AC024009

VERSION AC024009.2 GI:7210067

KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 182662)

AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.

TITLE Homo sapiens chromosome 2, clone RP11-158J14

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 182662)

AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,

Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavsky,L.,

Boukhalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,

Choepl,Y., Collangelo,M., Collins,S., Collymore,A., Cooke,P.,

Dearellano,K., Dewar,K., Dodge,S., Domino,M., Doyle,M.,

Fenestor,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D.,

Galagau,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,

Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,  
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,  
Klein,J., Landers,T., Largocque,K., Lehoczy,J., Levine,R.,  
Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M.,  
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Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C.,  
Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S.,  
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Subramanian,A., Talamas,J., Testaye,S., Theodore,J., Tirrell,A.,  
Travers,M., Triglio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B.,  
Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and  
Zody,M.

Direct Submission  
Submitted (20-FEB-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 182562)  
Hirren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,  
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Melidrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,  
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Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,  
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,  
Testaye,S., Theodore,J., Tirrell,A., Travers,M., Triglio,J.,  
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,  
Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission  
Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 8, 2000 this sequence version replaced gi:7008914.  
All repeats were identified using RepeatMasker:  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIGR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: 17216  
Center clone name: 158\_J\_14  
----- Summary Statistics  
Sequencing vector: M13; M77815; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
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Consensus quality: 171836 bases at least Q30  
Consensus quality: 176600 bases at least Q20  
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Insert size: 179762; sum-of-ctnigs  
Quality coverage: 3.9 in Q20 bases; agarose-fp  
Quality coverage: 3.9 in Q20 bases; sum-of-ctnigs  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 30 ctnigs, the true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the ctnigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will

\* be preserved.  
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38 137: gap of 100 bp  
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3193 3292: gap of 100 bp  
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* 53296 64559: contig of 11264 bp in length
* 64560 64659: gap of 100 bp
* 64660 79824: contig of 15165 bp in length
* 79825 79924: gap of 100 bp
* 79925 99909: contig of 19985 bp in length
* 99910 100009: gap of 100 bp
* 100010 121977: contig of 21968 bp in length
* 121978 122077: gap of 100 bp
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Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Search completed: March 11, 2003, 09:15:02  
 Job time : 8549.13 secs